-continued

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<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic nucleotide sequence.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: This nucleotide may have a 5' phosphate.

<400> SEQUENCE: 6

gatcggaaga gcgtcgtgta gggaaagagt gtagatctcg 40

<210> SEQ ID NO 7
<211> LENGTH: 48
<212> TYPE: DNA
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<223> OTHER INFORMATION: Nucleotides 42 to 47 may be any nucleotide.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (47)..(48)
<223> OTHER INFORMATION: There may be a phosphorothioate bond between
nucleotides 47 and 48.

<400> SEQUENCE: 7

cgagatctac actctttccc tacacgacgc tcttccgatc tnnnnnnt 48

<210> SEQ ID NO 8
<211> LENGTH: 47
<212> TYPE: DNA
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<220> FEATURE:
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<223> OTHER INFORMATION: Nucleotides 1 to 6 may be any nucleotide.
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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: This nucleotide may have a 5' phosphate.

<400> SEQUENCE: 8

nnnnnnagat cggaagagcg tcgtgtaggg aaagagtgta gatctcg 47

The invention claimed is:

1. A method for analyzing short tandem repeats (STRs), comprising:

(a) separately digesting, using an RNA-guided nuclease:

(i) a first portion of a genomic sample from an individual, at a defined site that is upstream of an STR; and

(ii) a second portion of the sample, at a defined site that is downstream of the STR, to produce first and second digestion products;

(b) fragmenting the first and second digestion products of step (a) to produce first and second fragmentation products;

(c) ligating an adaptor to the fragmentation products of step (b) to produce first and second ligation products;

(d) selectively amplifying, using strand-specific primers and a primer that hybridizes to the adaptor:

(i) part of the top strand but not the bottom strand of the first ligation products; and

(ii) part of the bottom strand but not the top strand of the second ligation products;

(e) sequencing at least some of the amplification products of step (d) to produce a plurality of top strand reads and a plurality of bottom strand reads; and

(f) counting the number of STR repeats in a sequence read of step (e), thereby providing an allele-specific count of the number of STR repeats at a particular locus in the genome of the individual.

2. The method of claim **1**, wherein the sequencing step (e) is paired-end sequencing, and wherein the method comprises, prior to said counting step (f), eliminating sequence reads that do not contain the sequence of a primer used in step (d).

3. The method of claim **1**, further comprising validating the number of STR repeats counted in (f) as being accurate only if the number matches the number of STR repeats counted in a read from the other strand.